

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 25, 2003, 14:40:41 ; Search time 12.7349 Seconds  
(Without alignments)  
837.928 Million cell updates/sec

Title: US-09-622-613b-26

Perfect score: 606  
Sequence: 1 NSMMATFOOKHIIIMPICN.....ICVKCENQYFVHFGIGRCP 111

Scoring table: BL0SUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	586.5	96.8	111	2	A27121
2	450	74.3	111	1	JX0120
3	369	60.9	111	2	JX0085
4	272.5	45.0	104	2	A39035
5	135.5	22.4	124	1	NRWHR
6	135.5	22.4	145	1	A35932
7	133.5	22.0	167	2	S20066
8	132.5	21.9	124	1	NRPG
9	126.5	20.9	119	2	S41111
10	122.5	20.2	124	1	NRPRH
11	122	20.1	122	1	NRKGR
12	120.5	19.9	128	1	NRCU
13	120.5	19.9	149	1	NRMS
14	119.5	19.2	123	1	A43825
15	118.5	19.6	128	1	NRGPB
16	117.5	19.4	128	1	NRHO
17	116.5	19.2	124	1	NRCM
18	116.5	19.2	124	1	NRCCM
19	116.5	19.2	124	1	NRCCM
20	116.5	19.2	128	1	NRKS
21	114.5	18.9	124	2	S08549
22	114	18.8	125	1	A32474
23	113.5	18.7	124	1	NRDEN
24	113.5	18.7	125	1	E43825
25	113	18.6	147	1	NRHUG
26	112.5	18.6	124	1	NRGF
27	112.5	18.6	124	1	NRDEO
28	111.5	18.4	130	2	S22808
29	110.5	18.2	124	1	NRBOB

30	110.5	18.2	124	1	NRWB	pancreatic ribonuc
31	110.5	18.2	124	1	NREKN	pancreatic ribonuc
32	110.5	18.2	124	2	S07141	pancreatic ribonuc
33	110.5	18.2	124	2	JC5560	pancreatic ribonuc
34	110.5	18.2	150	1	NRBO	pancreatic ribonuc
35	110.5	18.2	158	2	I61900	eosinophil-derived
36	109.5	18.1	124	1	NRSH	pancreatic ribonuc
37	108.5	17.9	119	2	JX0115	pancreatic ribonuc
38	108.5	17.9	124	1	NRCB	pancreatic ribonuc
39	108.5	17.9	152	1	NRRT	pancreatic ribonuc
40	106.5	17.6	124	1	NRHP	pancreatic ribonuc
41	106.5	17.6	125	4	A47498	pancreatic ribonuc
42	106.5	17.6	150	1	NRBOS	seminal ribonuclea
43	104.5	17.2	124	1	NRGN	pancreatic ribonuc
44	104.5	17.2	124	1	NRDF	pancreatic ribonuc
45	104	17.2	125	2	S04503	pancreatic ribonuc

## ALIGNMENTS

## RESULT 1

A27121  
Ribonuclease-related stalic acid-binding lectin - bullfrog  
C:Species: Rana catesbeiana (bullfrog)  
C:Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 30-Jun-1993  
C:Accession: A27121  
R:Tilani, K., Takio, K.; Kuwada, M.; Nitta, K.; Sakakibara, F.; Kawachi, H.; Takayan  
Biochemistry 26, 2189-2194, 1987  
A:Title: Amino acid sequence of stalic acid-binding lectin from frog (Rana catesbeiana)  
A:Reference number: A27121; MUID:87299649; PMID:3304421  
A:Accession: A27121  
A:Molecule type: protein  
A:Residues: 1-111 <TIT>  
C:Superfamily: pancreatic ribonuclease  
C:Keywords: lectin

Query Match 96.8%; Score 586.5; DB 2; Length 111;  
Best Local Similarity 99.1%; Pred. No. 2.6e-51;  
Matches 109; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 3 NMATFOOKHIIIMPICNTIMDNIIYVGQCKRVMTFIISATVKAICGVINNVL 61  
DB 2 NMATFOOKHIIIMPICNTIMDNIIYVGQCKRVMTFIISATVKAICGVINNVL 61  
OY 62 STTFQOLNCTRTSITPRCPYSRTETNYICVCEMOYFVHFGIGRCP 111  
DB 62 STTFQOLNCTRTSITPRCPYSRTETNYICVCEMOYFVHFGIGRCP 111

## RESULT 2

JX0120  
Ribonuclease-related stalic acid-binding lectin - Japanese frog  
C:Species: Rana japonica (Japanese frog)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: JX0120  
R:Kamitaya, Y.; Oyama, F.; Oyama, R.; Sakakibara, F.; Nitta, K.; Kawachi, H.; Takeyana  
J. Biochem. 108, 139-143, 1990  
A:Title: Amino acid sequence of a lectin from Japanese frog (Rana japonica) eggs.  
A:Reference number: JX0120; MUID:91035319; PMID:2229005  
A:Accession: JX0120  
A:Molecule type: protein  
A:Residues: 1-111 <KAM>  
C:Superfamily: pancreatic ribonuclease  
C:Keywords: lectin; pyroglyutamic acid  
F:1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental  
F:19-72,34-82,52-97,94-111/Disulfide bonds: #status experimental

Query Match 74.3%; Score 450; DB 1; Length 111;  
Best Local Similarity 78.2%; Pred. No. 9.2e-38;  
Matches 86; Conservative 7; Mismatches 15; Indels 2; Gaps 2;

OY 3 NMAFQOKHITMP-IICNTIMDNNTIYVGGCKRVNFTIISATVKAICTGY-IMNV 60  
 DB 2 NMAFQOKHITMP-IICNTIMDNNTIYVGGCKRVNFTIISATVKAICTGY-IMNV 61  
 OY 61 LSTTRPOLNCTRTSITPRCPYSSRTETNYICVCKENQPVHFAIGRC 110  
 DB 62 LSTTRPOLNCTRTSITPRCPYSSRTETNYICVCKENQPVHFAIGRC 111

## RESULT 3

JX0085  
 pancreatic ribonuclease (EC 3.1.27.5) - bullfrog  
 C:Species: Rana catesbeiana (bullfrog)  
 C>Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 05-Aug-1994  
 C:Accession: JX0085  
 R:Nitta, R.; Katsuyama, N.; Okabe, Y.; Iwama, M.; Watanabe, H.; Abe, Y.; Okazaki, T.; Ohg  
 J. Biochem. 106, 729-735, 1989  
 A:Title: Primary structure of a ribonuclease from bullfrog (Rana catesbeiana) liver.  
 A:Reference number: JX0085; MUID:90130374; PMID:2613682  
 A:Accession: JX0085  
 A:Molecule type: protein  
 A:Residues: 1-111 <NTT>  
 C:Superfamily: pancreatic ribonuclease  
 C:Keywords: hydrolase; pyroglyutamic acid  
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F:10/35/104/Active site: His, Lys, His #status predicted  
 F:19-72/34-82/52-97/94-111/Disulfide bonds: #status predicted

Query Match 60.9% Score 369; DB 2; Length 111;  
 Best Local Similarity 65.5%; Pred. No. 1e-29;  
 Matches 72; Conservative 9; Mismatches 27; Indels 2; Gaps 2;

OY 3 NMAFQOKHITMP-IICNTIMDNNTIYVGGCKRVNFTIISATVKAICTGY-IMNV 60  
 DB 2 NMAFQOKHITMP-IICNTIMDNNTIYVGGCKRVNFTIISATVKAICTGY-IMNV 61  
 OY 61 LSTTRPOLNCTRTSITPRCPYSSRTETNYICVCKENQPVHFAIGRC 110  
 DB 62 LSTTRPOLNCTRTSITPRCPYSSRTETNYICVCKENQPVHFAIGRC 111

## RESULT 4

A39035  
 ribonuclease-related anti-tumor protein - northern leopard frog (fragment)  
 C:Species: Rana pipiens (northern leopard frog)  
 C>Date: 31-Jul-1991 #sequence\_revision 31-Jul-1991 #text\_change 30-Jun-1993  
 C:Accession: A39035  
 R:Ardelet, W.; Mikulski, S.M.; Shogen, K.  
 J. Biol. Chem. 266, 245-251, 1991  
 A:Title: Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and earl  
 A:Reference number: A39035; MUID:91093131; PMID:1985896  
 A:Accession: A39035  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-104 <ARD>  
 C:Superfamily: pancreatic ribonuclease

Query Match 45.0% Score 272.5; DB 2; Length 104;  
 Best Local Similarity 49.1%; Pred. No. 3.6e-20;  
 Matches 54; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

OY 3 NMAFQOKHITMP-IICNTIMDNNTIYVGGCKRVNFTIISATVKAICTGY-IMNV 60  
 DB 2 NMAFQOKHITMP-IICNTIMDNNTIYVGGCKRVNFTIISATVKAICTGY-IMNV 61  
 OY 61 LSTTRPOLNCTRTSITPRCPYSSRTETNYICVCKENQPVHFAIGRC 110  
 DB 58 LSTTRPOLNCTRTSITPRCPYSSRTETNYICVCKENQPVHFAIGRC 104

## RESULT 5

NRMHK  
 pancreatic ribonuclease (EC 3.1.27.5) - minke whale

N:Alternate names: RNase 1; RNase A  
 C:Species: Balaenoptera acutorostrata (minke whale, lesser rorqual)  
 C>Date: 24-Apr-1984 #sequence\_revision 24-Apr-1984 #text\_change 03-Jun-1994  
 C:Accession: A00818  
 R:Emmens, M.; Wellings, G.W.; Beintema, J.J.  
 Biochem. J. 157, 317-323, 1976  
 A:Title: The amino acid sequence of pike whale (lesser rorqual) pancreatic ribonuclea  
 A:Reference number: A00818; MUID:76277855; PMID:962870  
 A:Accession: A00818  
 A:Molecule type: protein  
 A:Residues: 1-124 <EMM>  
 C:Superfamily: pancreatic ribonuclease  
 C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas  
 F:12/41/119/Active site: His, Lys, His #status predicted  
 F:26-84/40-95/58-110/65-72/Disulfide bonds: #status predicted  
 F:76/Binding site: carbohydrate (asn) (covalent) (partial) #status experimental

Query Match 22.4% Score 135.5; DB 1; Length 124;  
 Best Local Similarity 33.3%; Pred. No. 1.7e-06;  
 Matches 39; Conservative 16; Mismatches 39; Indels 23; Gaps 7;

OY 7 FQOKHITMP-IICNTIMDNNTIYVGGCKRVNFTIISATVKAICTGY-IMNV 60  
 DB 8 FQOKHITMP-IICNTIMDNNTIYVGGCKRVNFTIISATVKAICTGY-IMNV 61  
 OY 61 LSTTRPOLNCTRTSITPRCPYSSRTETNYICVCKENQPVHFAIGRC 110  
 DB 64 LCKNGRTNCEYNSNTHIITDCRGTGSSKRYNCATKTSQKKEHIIIVACENGPIYPVHF 120

## RESULT 6

A35932  
 angiotensin precursor - mouse  
 N:Alternate names: angiotensin factor  
 C:Species: Mus musculus (house mouse)  
 C>Date: 09-Nov-1990 #sequence\_revision 09-Nov-1990 #text\_change 18-Jun-1999  
 C:Accession: A35932  
 R:Bond, M.D.; Vallée, B.L.  
 Biochem. Biophys. Res. Commun. 171, 988-995, 1990  
 A:Title: Isolation and sequencing of mouse angiotensin DNA.  
 A:Reference number: A35932; MUID:91025023; PMID:2222458  
 A:Accession: A35932  
 A:Status: not compared with conceptual translation  
 A:Molecule type: DNA  
 A:Residues: 1-145 <BON>  
 A:Cross-references: GB:022516; NID:9726325; PIDN:AAA91366.1; PID:9726326  
 C:Genetics:  
 A:Introns: #status absent  
 C:Function:  
 A:Description: hydrolyzes tRNA; induces vascularization of normal and malignant tissu  
 C:Superfamily: pancreatic ribonuclease  
 C:Keywords: angiogenesis; hydrolase; nucleic acid degradation; pyroglyutamic acid  
 F:1/24/Domin: signal sequence #status predicted <SIG>  
 F:25/145/Product: angiotensin #status predicted <MAT>  
 F:25/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predic  
 F:37/64/137/Active site: His, Lys, His #status predicted  
 F:50-104/63-115/61-130/Disulfide bonds: #status predicted

Query Match 22.4% Score 135.5; DB 1; Length 145;  
 Best Local Similarity 39.5%; Pred. No. 2e-06;  
 Matches 30; Conservative 12; Mismatches 29; Indels 5; Gaps 3;

OY 34 KRNFTPIISATVKAICTGY-IMNV-LSSTTRPOLNCTRTSITPR-PPYSSRTE 88  
 DB 63 KRNFTPIISATVKAICTGY-IMNV-LSSTTRPOLNCTRTSITPR-PPYSSRTE 89  
 OY 89 TNYICVCKENQPVHFAIGRC 104  
 DB 123 FRHVIIVACENGPIYPVHF 138

## RESULT 7

```

C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F:12/41,119/Active site: His, Lys, His #status predicted
F:21/34,76/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:26-84,40-95,58-110,65-72/Disulfide bonds: #status experimental

Query Match          21.9%: Score 132.5; DB 1; Length 124;
Best Local Similarity 31.6%: Pred. No. 3.5e-06;
Matches 36; Conservative 19; Mismatches 42; Indels 17; Gaps 6;

OY 7 FQAKHI-----IMPPLICNTIMDNNTIYVGCKRVWTFPIISATTVKACTGV-INMN 59
      ||::||  ::::  ||  ::  ::::  ::::  ::::  ::::  ::::  ::::  ::::
DB 8 FQKHDDSSSSNSNNCNLMMSRR-NMTGGRCKPVNTFVHESLADVAQVCSILNNCK 66
      ||::||  ::::  ||  ::  ::::  ::::  ::::  ::::  ::::  ::::
OY 60 VLSITRQLNT-----CTRTSITPRP-CPTSSRTENNYCYKRENG--YPIYR 104
      ||::||  ::::  ||  ::  ::::  ::::  ::::  ::::  ::::  ::::
DB 67 NGQNTCYOSNTSMHTITDCKRTGSSSKYPCAKVASEQKHIIIVACEGNPVPVYR 120
      ||::||  ::::  ||  ::  ::::  ::::  ::::  ::::  ::::  ::::

RESULT 9
S41111
pancreatic ribonuclease - common Iguana
C:Species: Iguana Iguana (common Iguana)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Aug-1998
C:Accession: S41111
R:Zhao, W.; Beintema, J.J.; Hofsteenge, J.
Eur. J. Biochem. 219, 641-646, 1994
A:Title: The amino acid sequence of iguana (Iguana Iguana) pancreatic ribonuclease.
A:Reference number: S41111; MUID:94139745; PMID:8307028
A:Accession: S41111
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-119 <ZNA>
C:Superfamily: pancreatic ribonuclease

Query Match          20.9%: Score 126.5; DB 2; Length 119;
Best Local Similarity 29.8%: Pred. No. 1.3e-05;
Matches 34; Conservative 16; Mismatches 51; Indels 13; Gaps 4;

OY 3 NMATFQOQHI-----INPFLICNTIMDNNTIYVGCKRVWTFPIISATTVKACTGV-INMN 52
      ||::||  ::::  ||  ::  ::::  ::::  ::::  ::::  ::::  ::::  ::::
DB 2 DMSRQNNKHIDYPRFSASNPAYCDLMMQR-NLNPTRCKRNTFVHASPFIQYQVCGSG 60
      ||::||  ::::  ||  ::  ::::  ::::  ::::  ::::  ::::  ::::  ::::
OY 53 -TGVINNVNSTTRPQLNTCTRTSIT-PRCPYSSRFETNYCYKCENQYPIYR 104
      ||::||  ::::  ||  ::  ::::  ::::  ::::  ::::  ::::  ::::  ::::
DB 61 GTHEEDNLVDNNESEFDLTDCKNVGTA PSSCKYNGTPTGTRIRIRIACENNQPVYR 114
      ||::||  ::::  ||  ::  ::::  ::::  ::::  ::::  ::::  ::::  ::::

RESULT 10
NRPRH
pancreatic ribonuclease (EC 3.1.27.5) - pronghorn (tentative sequence)
N:Alternate names: RNase 1; RNase A
C:Species: Antilocapra americana (pronghorn)
C:Date: 28-Feb-1981 #sequence_revision 28-Feb-1981 #text_change 31-Mar-2000
C:Accession: A00813
R:Beintema, J.J.; Gaestle, W.; Munnikema, J.
J. Mol. Evol. 13, 305-316, 1979
A:Title: Primary structure of pronghorn pancreatic ribonuclease: close relationship b
A:Reference number: A00813; MUID:80075014; PMID:513141
A:Accession: A00813
A:Molecule type: protein
A:Residues: 1-124 <BRT>
C:Superfamily: pancreatic ribonuclease
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F:12/41,119/Active site: His, Lys, His #status predicted
F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
F:34/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental

Query Match          20.2%: Score 122.5; DB 1; Length 124;
Best Local Similarity 30.3%: Pred. No. 3.4e-05;
Matches 36; Conservative 18; Mismatches 42; Indels 23; Gaps 7;

OY 5 ATFOQKHINPPI-----ICNTIMDNNTIYVGCKRVWTFPIISATTVKACTGV-INMN 58
      ||::||  ::::  ||  ::  ::::  ::::  ::::  ::::  ::::  ::::  ::::

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Db 6 AKERHIDNSPSSVSSNNCNOMKSR-NLTGRCRPVTFHESLADVOAVCS---QK 61  
 59 NVL-----STTRFQNLNCTRTSTITPRP-CPYSSRTETNYCKCE-NQY-PVHF 104  
 Db 62 NVACKNGOTNCYQYSMTSIDCRETGSSKRPVNTTQAKKHITVACGEGNPVPHY 120

RESULT 11  
 NRKRK  
 pancreatic ribonuclease (EC 3.1.27.5) - red kangaroo  
 N:Alternate names: RNase A  
 C:Species: Macropus rufus, Megaleia rufa (red kangaroo)  
 C>Date: 30-Nov-1980 #sequence\_revision 30-Nov-1980 #text\_change 04-Oct-1996  
 C:Accession: A00833  
 R:Gastra, W.; Welling, G.W.; Beintema, J.J.  
 Eur. J. Biochem. 86, 209-217, 1978  
 A:Title: The amino-acid sequence of kangaroo pancreatic ribonuclease.  
 A:Reference number: A00833; MUID:78190621; PMID:658039  
 A:Accession: A00833  
 A:Molecule type: protein  
 A:Residues: 1-122 <GAA>  
 C:Superfamily: pancreatic ribonuclease  
 C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas  
 F:11,40,117/Active site: His, Lys, His #status predicted  
 F:23-83,39-94,57-109,64-71/Disulfide bonds: #status predicted  
 F:61/Binding site: carbohydrate (Asn) (covalent) #status absent

Query Match 20.1%; Score 122; DB 1; Length 122;  
 Best Local Similarity 30.7%; Pred. No. 3.8e-05;  
 Matches 35; Conservative 16; Mismatches 45; Indels 18; Gaps 6;

7 FQOKHI-----INTPLICNTIMDNNTIYVGGCKRVNFTLISSATVKAIC----- 52  
 Db 7 FORGHMDPSTSSSSVNCNLMKAR-DMTSGRCKPLNFTHEPKSVYDAVACHENVTCK 65  
 53 TGVINMNVLTSTRFQNLNCTRTSTITPRP-CPYSSRTETNYCKCE-NQY-PVHF 104  
 Db 66 NGRTNC-YKSNRSLSTNCRGTGASKYPCOYERSNLTQIVACGQVYPVHF 118

RESULT 12  
 NRCU  
 pancreatic ribonuclease (EC 3.1.27.5) - nutria (tentative sequence)  
 N:Alternate names: RNase 1; RNase A  
 C:Species: Myocastor coypus (nutria, coypu)  
 C>Date: 24-Apr-1984 #sequence\_revision 30-Sep-1988 #text\_change 31-Mar-2000  
 C:Accession: A00832  
 R:van den Berg, A.; van den Hende-Timmer, L.; Beintema, J.J.  
 Biochim. Biophys. Acta 453, 400-409, 1976  
 A:Title: Isolation, properties and primary structure of coypu and chinchilla pancreatic  
 A:Reference number: A90612; MUID:77065676; PMID:995896  
 A:Accession: A00832  
 A:Molecule type: protein  
 A:Residues: 1-126 <VAN>  
 C:Superfamily: pancreatic ribonuclease  
 C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas  
 F:11,41,119/Active site: His, Lys, His #status predicted  
 F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted  
 F:34/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 19.9%; Score 120.5; DB 1; Length 128;  
 Best Local Similarity 31.6%; Pred. No. 5.6e-05;  
 Matches 37; Conservative 15; Mismatches 42; Indels 23; Gaps 7;

7 FQOKHI-----INTPLICNTIMDNNTIYVGGCKRVNFTLISSATVKAICGVIMNV 60  
 Db 8 FERQHMDSPSTNPTNYCNEMKSR-NMTGRCRKPNTVHEPLADVOAVC---FQKNV 63  
 61 L-----STTRFQNLNCTRTSTITPRP-CPYSSRTETNYCKCE-NQY-PVHF 104  
 Db 64 LCKNGOTNCYQYSNMHITDCRVTNSDYPNCSVRTSQEKSIVACGEGNPVPHF 120

RESULT 13  
 NRMS  
 pancreatic ribonuclease (EC 3.1.27.5) precursor - mouse

N:Alternate names: RNase 1; RNase A  
 C:Species: Mus musculus (house mouse)  
 C>Date: 30-Nov-1980 #sequence\_revision 13-Mar-1997 #text\_change 18-Jun-1999  
 C:Accession: A34090; S22598; A00830  
 R:Schueller, C.; Nijssen, H.M.J.; Kok, R.; Beintema, J.J.  
 Mol. Biol. Evol. 7, 29-44, 1990  
 A:Title: Evolution of nucleic acids coding for ribonucleases: the mRNA sequence of mo  
 A:Reference number: A34090; MUID:90136034; PMID:2259980  
 A:Accession: A34090  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-149 <SCCH>

A:Cross-references: CB:M27814; NID:g200762; PION:AAA0060.1; PID:g200763  
 R:Samuelson, L.C.; Wiebauer, K.; Howard, G.; Schmid, R.M.; Koepf, D.; Mettler, M.H.  
 Nucleic Acids Res. 19, 6935-6941, 1991  
 A:Title: Isolation of the murine ribonuclease gene R1b-1: structure and tissue specif  
 A:Reference number: S22598; MUID:92107684; PMID:1840677  
 A:Accession: S22598  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-149 <SAM>  
 A:Cross-references: EMBL:X60103; NID:g53981; PID:CAA42697.1; PID:g53982  
 R:Lenstra, J.A.; Beintema, J.J.  
 Eur. J. Biochem. 98, 399-408, 1979  
 A:Title: The amino acid sequence of mouse pancreatic ribonuclease.  
 A:Reference number: A00830; MUID:80024269; PMID:556267  
 A:Accession: A00830  
 A:Molecule type: protein  
 A:Residues: 26-149 <LEN>

C:Superfamily: pancreatic ribonuclease  
 C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas  
 F:1-25/Domain: signal sequence #status predicted <IG>  
 F:26-149/Product: pancreatic ribonuclease #status predicted <MA>  
 F:37,66,144/Active site: His, Lys, His #status predicted  
 F:51-109,65-120,83-135,90-97/Disulfide bonds: #status predicted  
 F:62,87/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 19.9%; Score 120.5; DB 1; Length 149;  
 Best Local Similarity 30.8%; Pred. No. 6.5e-05;  
 Matches 36; Conservative 16; Mismatches 42; Indels 23; Gaps 7;

7 FQOKHI-----INTPLICNTIMDNNTIYVGGCKRVNFTLISSATVKAICGVIMNV 60  
 Db 33 FORGHMDPSSSSVNCNLMKAR-DMTSGRCKPLNFTHEPKSVYDAVACHENVTCK 65  
 61 L-----STTRFQNLNCTRTSTITPRP-CPYSSRTETNYCKCE-NQY-PVHF 104  
 Db 89 TCKNRKNCYKSSALHITDCHLKGNSKYPNCVKTQYOKKHITVACGEGNPVPHF 145

RESULT 14  
 A43825  
 angiotensin - pig  
 C:Species: Sus scrofa domestica (domestic pig)  
 C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C:Accession: S29834; A43825  
 R:Bond, M.D.; Strydom, D.J.; Vallee, B.L.  
 Biochim. Biophys. Acta 1162, 177-186, 1993  
 A:Title: Characterization and sequencing of rabbit, pig and mouse angiotensins: discer  
 A:Reference number: S29833; MUID:93192291; PMID:8448182  
 A:Accession: S29834  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-123 <BN>  
 A>Note: this sequence was submitted to the Protein Sequence Database, December 1992  
 C:Superfamily: pancreatic ribonuclease

Query Match 19.7%; Score 119.5; DB 1; Length 123;  
 Best Local Similarity 39.5%; Pred. No. 6.7e-05;  
 Matches 30; Conservative 6; Mismatches 35; Indels 5; Gaps 2;

OY 34 CKRNFPIISSATTKAICTG---VINNVNLTSTRPOLNTCTRTSITPR-PCPYSSRTE 88  
 DB 39 CKRNFPIHCFGRNDIKACNDKNGEPYNNFRRSKSPQITTCYKHKGGSNRPCCYRATAG 98  
 OY 89 TNYICVCKENQYPPVHF 104  
 DB 99 FRTIIVACENGGLPVPVHF 114

## RESULT 15

NRGPB

pancreatic ribonuclease (EC 3.1.27.5) B - guinea pig (tentative sequence)

N:Alternate names: RNase1B

C:Species: Cavia porcellus (guinea pig)

C&gt;Date: 24-Apr-1984 #sequence, revision 24-Apr-1984 #text, change 31-Mar-2000

C:Accession: A00826

R:van den Berg, A.; van den Hende-Timmer, L.; Hofsteenge, J.; Gaasstra, W.; Beintema, J.

Eur. J. Biochem. 75, 91-100, 1977

A:Title: Guinea pig pancreatic ribonucleases. Isolation, properties, primary structure

A:Reference number: A91247; PMID:77185023; PMID:862624

A:Accession: A00826

A:Molecule type: protein

A:Residues: 1-128 &lt;VAN&gt;

A&gt;Note: 64-Pro was also found

C:Superfamily: pancreatic ribonuclease

C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas

F;12,41,119/active site; His, Lys, His #status predicted

F;21,34/Binding site: carbohydrate (asn) (covalent) #status experimental

F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted

Query Match 19.6%; Score 118.5; DB 1; Length 128;

Best Local Similarity 31.6%; Pred. No. 8.8e-05;

Matches 37; Conservative 14; Mismatches 43; Indels 23; Gaps 6;

OY 7 FQOKH-----INPIICNTIMDNIIYIGQCKRVNFISSATTKAICTGVINNV 60  
 DB 8 FORQHMDEKSPSPNSNYCNVMMIR-NMTQGRCKPVNPFVHESLADYQAVC---FQKNV 63  
 OY 61 L-----STTRQALNTCTRTSITPRP-CYSSRTETNYICVCKENO--YPPVHF 104  
 DB 64 LCKNKQTNCYQSYSRMRITDCRYTSSSKFPNCYSRMSQAKSIIIVACEGDDPYVPVHF 120

Search completed: June 25, 2003, 14:58:07  
 Job time: 13.7349 secs

